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Supplemental Information

Genomic and Strontium Isotope Variation

Reveal Immigration Patterns in a Viking Age Town

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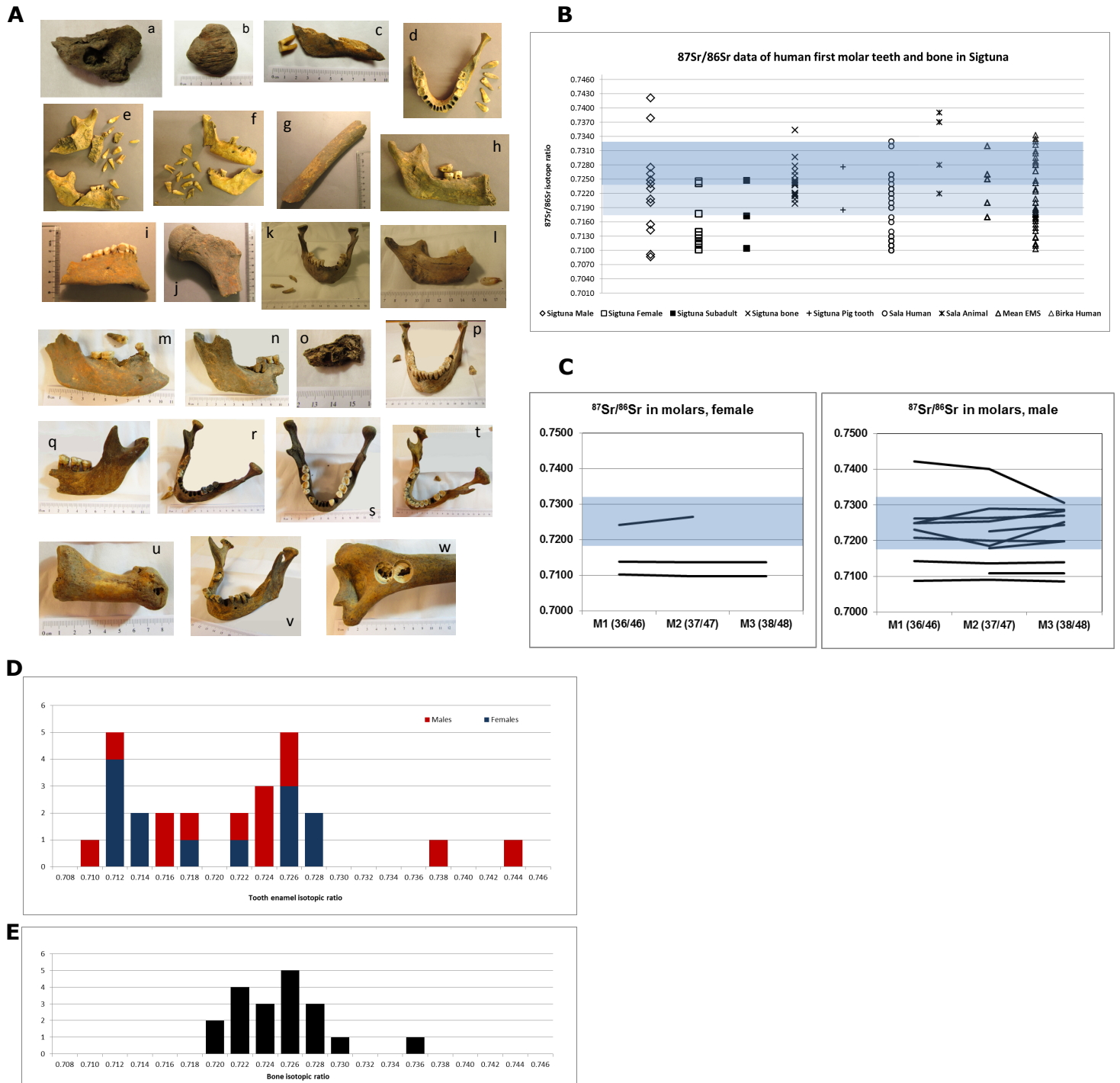


Figure S1. Skeletal material and strontium isotope results. Related to Figure 3.

(A) Skeletal material analysed in this study; a: bns023; b: grt035; c: grt036; d: 84001; e: 84005; f: 84035; g: 97002; h: 2072; i: 97026; j: 97029; k: gtm021; l: gtm127; m: kal006; n: kal009; o: kls001; p: nuf002; q: stg020; r: stg021; s: stg026; t: urm035; u: urm045; v: urm160; w: urm161. **(B)** $^{87}\text{Sr}/^{86}\text{Sr}$ isotope ratios of human first molars and bone and two faunal samples from Sigtuna. The shaded range corresponds to the estimated local base line between 0.717-0.732. One bone value is considered to be an outlier, probably related to diagenesis. Values for Sala were collected from Bäckström & Price (2016) [S1] and for Early Medieval Sweden (EMS) are from Price et al. (2015) [S2]. Data in Table S1. **(C)** $^{87}\text{Sr}/^{86}\text{Sr}$ isotope ratios of human molars (M1, M2 and M3) from Sigtuna. The shaded range corresponds to the estimated local baseline between 0.717-0.732. Data for three females and eleven males, data in Table S1. Distribution of $^{87}\text{Sr}/^{86}\text{Sr}$ isotope ratios in 26 females and males (M1) from Sigtuna **(D)** and the distribution of $^{87}\text{Sr}/^{86}\text{Sr}$ data of 17 human bones and two pig teeth (enamel) from Sigtuna **(E)**.

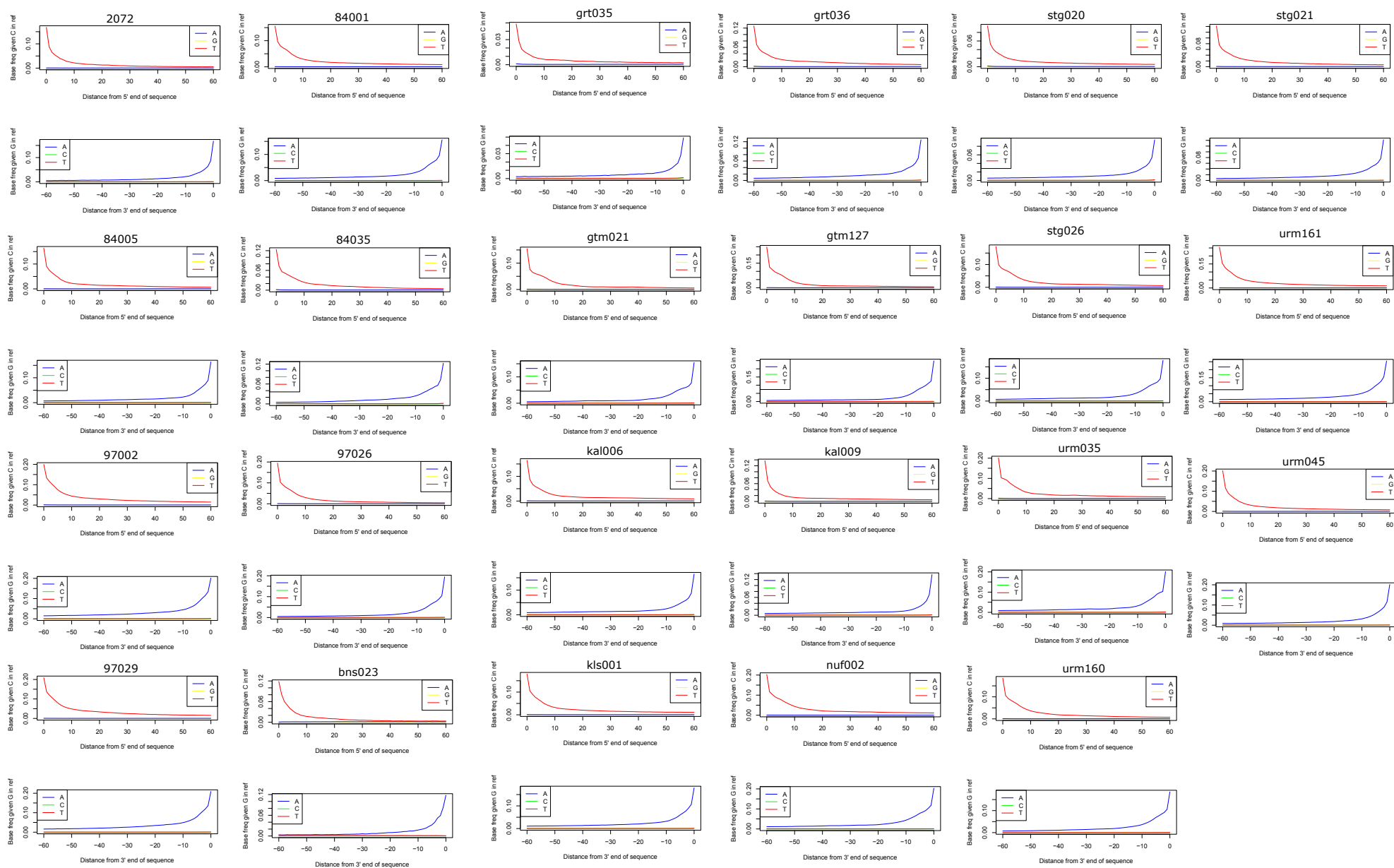


Figure S2. Deamination patterns in ancient individuals. Related to Figure 2, Figure 3 and Table 1.

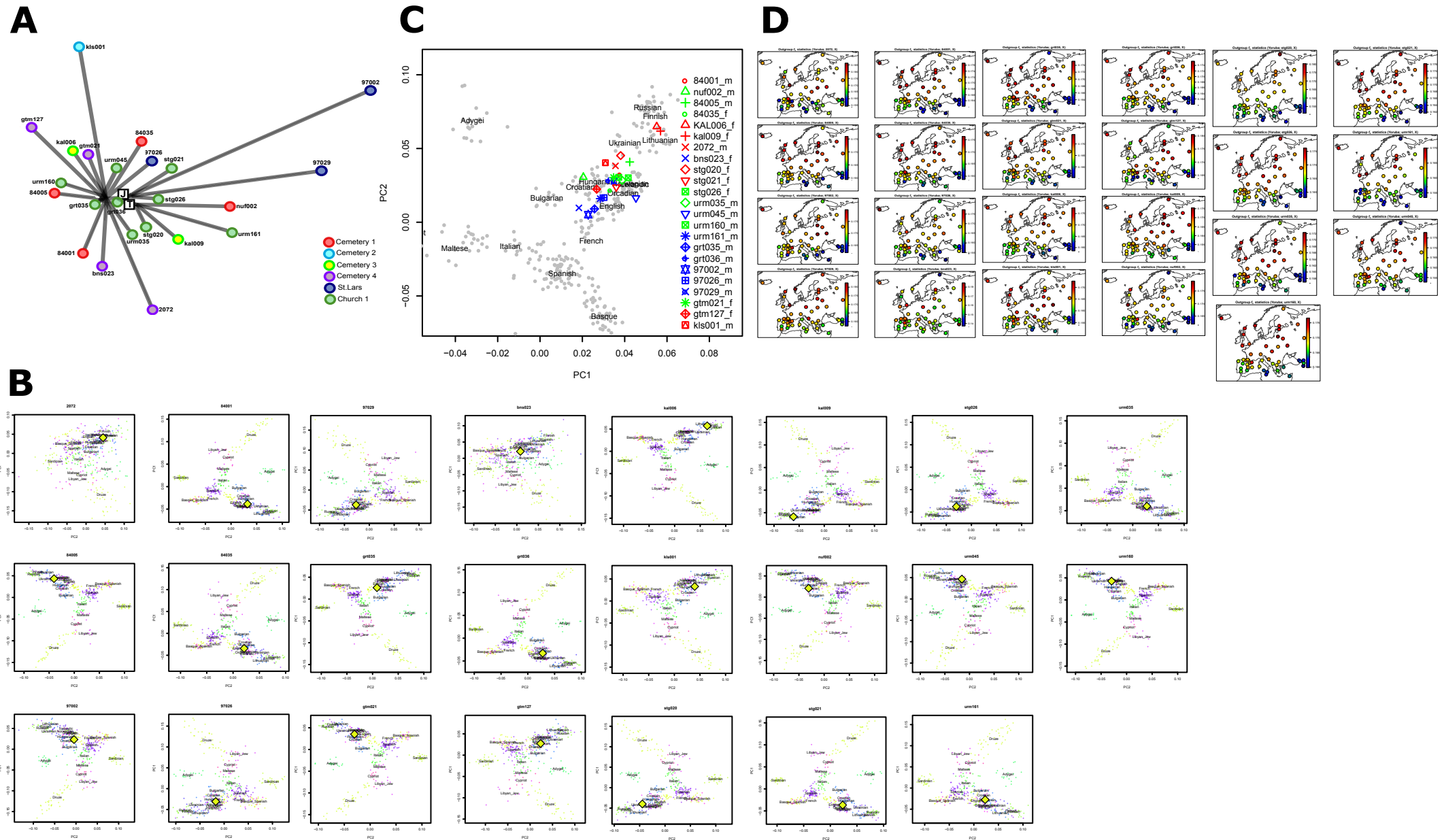


Figure S3. Mitochondrial network analyses, combined and individual PCA plots and f_3 -statistics results. Related to Figure 2, Figure 3 and Table 1.

(A) Network analyses of mtDNA genomes from ancient individuals from Sigtuna. The colours represent individual burial grounds.

(B) Individual PCA plots for tested individuals. **(C)** A PCA plot visualising all 23 individuals from Sigtuna used in ancient DNA analyses (m - males, f - females). **(D)** Outgroup f_3 -statistic for all individuals in this study.

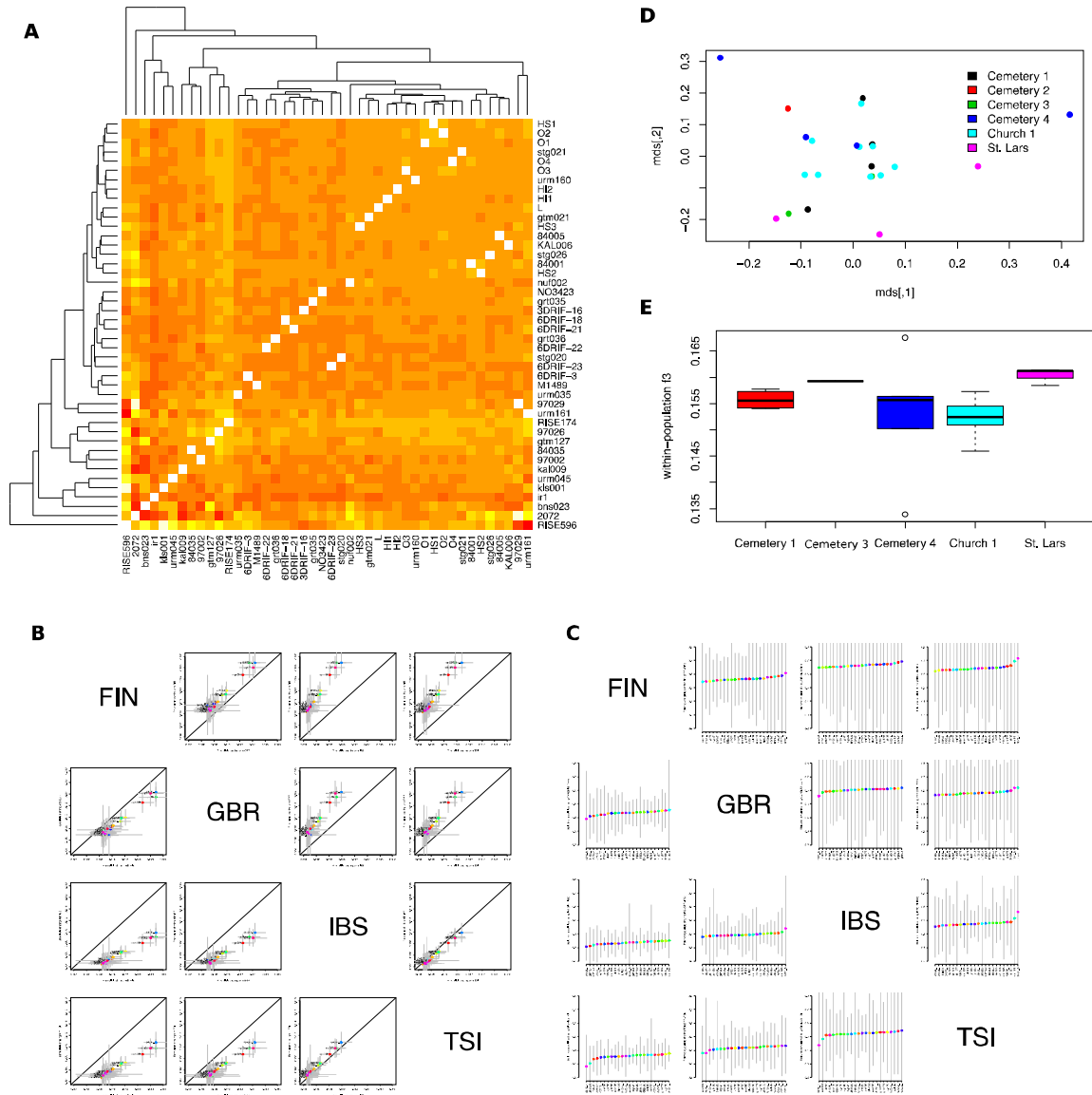


Figure S4. Pair-wise f_3 value compositions and rare allele sharing. Related to Figure 2, Figure 3 and Table 1

(A) Heat map of f_3 -outgroup statistic values between pairs of various ancient individuals tested. (B) Relative rare allele sharing between all tested individuals and four test populations from the 1000 Genomes Project. The vertical error bars show two standard errors. (C) Rare allele sharing ratios between all tested individuals and four test populations from the 1000 Genomes Project. The vertical error bars show two standard errors. (D) Distance matrix MDS plot of pairwise f_3 values calculated between individuals from Sigtuna. (E) Within group variation of pair-wise f_3 values in five burial sites in Sigtuna. Cemetery 2 represented by one individual was removed from the analysis.

Cemetery*	ID	Sex	⁸⁷ Sr/ ⁸⁶ Sr data								Comment
			DNA Code	DNA sample source	Age	Dating	First molar (36/46)	Second molar (37/47)	Third molar (38/48)	Bone	
Cemetery 1 (Nunnan)	84001	M	84001	C mand sin	M	1055 ±30BP Ua-	0.7143	0.7136	0.714	0.7246	
Cemetery 1 (Nunnan)	84012	M			A			0.7179	0.7198	0.7258	
Cemetery 1 (Nunnan)	84005	M	84005	C mand dx	A		0.7248	0.7253	0.7283	0.7266	
Cemetery 1 (Nunnan)	84002	M	nuf002	M3 sin	A		0.7201				
Cemetery 1 (Nunnan)	84035	F	84035	C mand dx	M	1155 ±30BP Ua-		0.7261			
Cemetery 2 (Kålsängen)	5002	M	kls001	Pars petrosa sin	A		0.7155				
Cemetery 3 (Källandet)	7006	F	kal006	PM2 mand dx	20+		0.7139	0.7137	0.7137	0.7248	M1=Inc **
Cemetery 3 (Källandet)	7009	F	kal009	PM1 mand dx	M		0.7115				
Cemetery 4 (Bensinstat.)	8072	M	2072	M3 mand sin	A	1056 ±35 BP Ua-	0.7422	0.7401	0.7306	0.7296	
Cemetery 4 (Bensinstat.)	8023	-	bns023	Pars petrosa sin	Infant	1060 ±35 BP Ua-				0.7278	F(DNA)
Cemetery 4 (Götes mack)	14004	M			A		0.7248	0.729	0.7286		
Cemetery 4 (Götes mack)	14006	M			M		0.7261	0.7264	0.7271		
Cemetery 4 (Götes mack)	14019	M			A		0.7275	0.7292	0.7208		
Cemetery 4 (Götes mack)	14029	M			A		0.7208	0.7199	0.7197		
Cemetery 4 (Götes mack)	14026	M			A		0.723	0.7185	0.7252		
Cemetery 4 (Götes mack)	14011	-			12-15		0.7104				M1=Can ***
Cemetery 4 (Götes mack)	14021	F	gtm021	C	M		0.7242	0.7264			
Cemetery 4 (Götes mack)	14027	F	gtm127	C	M		0.7102	0.7098	0.7098		
Church 1 (St.Gertrud)	93019	-			17-22		0.7247	0.7277			
Church 1 (St.Gertrud)	83020	F	stg020	Mand sin	A		0.7132				
Church 1 (St.Gertrud)	83021	F	stg021	Mand	A	1020 ±35 BP Ua-	0.7112				
Church 1 (St.Gertrud)	83025	F			A		0.7119				F(DNA) ****
Church 1 (St.Gertrud)	83026	F	stg026	Mand	20+	1115 ±35 BP Ua-	0.7246				
Church 1 (St.Gertrud)	95035	M	grt035	Patella sin	20+	1080 ±40 BP Ua-				0.722	
Church 1 (St.Gertrud)	95036	M	grt036	Mand dx	M	985 ±35 BP Ua-22734				0.7242	
Church 1 (Urmakaren)	90035	M	urm035	Mand dx/sin	M	975 ±35BP Ua-22733		0.7226	0.7243	0.7221	
Church 1 (Urmakaren)	90045	-	urm045	Mt1 dx							
Church 1 (Urmakaren)	90160	M	urm160	Mand dx/sin	M	885 ±35BP Ua-22740		0.7234		0.7243	
Church 1 (Urmakaren)	90161	M	urm161	Humerus sin	I	965 ±35BP Ua-22741					
Church 1 (Urmakaren)	90070	M			A		0.7086	0.709	0.7085	0.7199	
Mass grave (St.Lars)	97025	-			c. 8	1115 ±29 BP	0.7172			0.7238	F(DNA) ****
Mass grave (St.Lars)	97015	M			A	(Ua-17743-Ua-17747)	0.7092			0.7208	
Mass grave (St.Lars)	97011	M			M			0.7108	0.7108	0.7217	

Mass grave (St.Lars)	97016	F			A		0.7177			0.7239	
Mass grave (St.Lars)	97002	M	97002	Femur dx	16-22					0.7215	
Mass grave (St.Lars)	97027	M			A		0.7379				
Mass grave (St.Lars)	97029	M	97029	Femur sin	16-22		0.7241				
Mass grave (St.Lars)	97026	M	97026	C mand dx	A					0.7354	
Humlegården	Pig						0.7185				Tooth
Sigtuna St.Lars	Pig						0.7276				Tooth

M= male, F= female; A= Adultus 20-40 years; M= Maturus 40+, C= complete (90-100%) skeleton, AC= almost complete (50-90%) skeleton, I= incomplete (<50%) skeleton; Dates within parenthesis= other skeletons from the same site; *No strontium data available for individuals urm045 (90045) and urm161 (90161), **Incisive studied instead of M1, ***Canine studied instead of M1, ****Sex assessment, Female, based on DNA.

Table S1. List of analyzed burials and individuals, including summary of osteological, archaeological and burial contexts and $^{87}\text{Sr}/^{86}\text{Sr}$ isotope ratios. Related to Table 1, Figure 1 and Figure 3. The isotope ratios were measured in 36 human tooth enamel and bone and two pig tooth enamel from Sigtuna (sin= left; dx= right; mand= mandible; M1/M2/M3= first/second/third molar; PM1/PM2= first/second premolar; Inc= incisor; C= canine; Mt1= first metatarsal; F(DNA)=female according to the genetic analysis).

ARTEFACT	REGION OF PROVENANCE*	REFERENCE
Prestige objects		
Glass beaker (Late Roman)	Black Sea region/Syria	[S3]
Glass beaker (Paphos-type)	Byzantine Empire	[S3]
Salt containers	West Slav region, Central Europe	[S4]
Ivory combs	Byzantine Empire	[S5]
Dress, personal items		
Temple rings	West Slav region	[S6,S7]
Enamelled cross brooches	Ottonian kingdom/Holy Roman Empire	[S8]
Glass finger rings	West Slav region	[S6]
Gold pendant Hiddensee-style	Danish realm	[S9,S10]
Patix for producing Mammen-style round brooches	Danish realm	[S9,S10]
Religious objects		
Crozier	Anglo-Norman region	[S11]
Baptismal font (fragment)	England/Sigtuna	[S12]
Sepulchral stones	Carolingian Germany	[S13]
Resurrection eggs	Kiev Rus'	[S14,S15]
Encolpion	Byzantine Empire	[S16]
Everyday use (tools and ceramics)		
Ceramics	West Slav region	[S7,S8]
Ceramics	Kiev Rus'	[S7,S8]
Baltic ware ceramics	East Slav region	[S17]
Amphoras	Black Sea region, Byzantine Empire, Kiev Rus'	[S7]
Spindle whorls, Volhynian type	Kiev Rus'	[S18]
Trade and means of payment		
Coins	Ottonian kingdom/Holy Roman Empire	[S19]
Coins	Frankish kingdom	[S19]
Coins (Ethelred II)	Anglosaxon	[S20]
Named minters	Sigtuna/Anglo-Saxon England	[S19]
Runestones mentioning guilds	Friesland	[S8] (U 379, U 391)
Lead seals	Byzantine Empire	[S21]

*site of manufacturing or region of influence

Table S2. Examples of artefacts and their region of provenance dated to the late 10th to the 12th century. Related to Figure 3.

Sample ID	Percentage of human DNA	Genome coverage	MtDNA genome coverage	Clonality	Mol. sex	MtDNA haplogroup	Y chromosome haplogroup	SNPs in HO	MtDNA contamination estimate	Male X-chr based contamination est. Method 1 (SE)	Male X-chr based contamination est. Method 2 (SE)
2072	0.6%	x 0.01	x 1.5	3.8	XY	U	Nd	>5k	-	6.61e-05 (0)	6.61E-05 (0)
84001	57.7%	x 3.7	x 108.2	3.7	XY	H2a2a1g	N1a1a1a1a1	>368k	0.15% (0.0-0.46%)	0.00844 (0.00068)	0.00712 (0.001011)
84005	20.1%	x 1.03	x 132.2	4.9	XY	H1ap1	I1a1b3	>269.3k	1.0% (0.13-1.89%)	0.00328 (0.00101)	0.00290 (0.000935)
84035	6.3%	x 0.2	x 149.6	40.9	XX	H2a3a	-	>81.4	0.5% (0.31-2.73%)		
97002	1.4%	x 0.12	x 27.7	49.7	XY	J2a1a (60%)	R1b	>46.5k	0.46% (0.0-1.37%)	0.00279 8(.00168)	0.00209 (0.001505)
97026	0.8%	x 0.08	x 87.6	13.8	XY	U5a2a1	Nd	>33.6k	0.0% (0.0-1.09%)	0.00118 (0.0012)	6.61E-05 (0)
97029	0.8%	x 0.07	x 34.2	36.1	XY	J1c2	Nd	=32k	0.40% (0.0-1.19%)	0.00681 (0.00297)	0.00451 (0.002357)
bns023	7.4%	x 0.02	x 3.7	11.7	XX	H4a1a3a	-	> 7.2k	-		
grt035	33.4%	x 3.2	x 279	37.3	XY	H	G2a2	>368.8k	0.0% (0.0-0.45%)	0.00166(0.0003171)	0.00085 (0.000361)
grt036	33.7%	x 2.2	x 247.8	49.1	XY	H13a1a5	I2a2/	>341.1k	0.23% (0.0-0.45%)	0.00705 (0.000660)	0.00457 (0.000729)
gtm021	54.5%	x 0.43	x 34.1	1.3	XX	H5	-	>150.6k	0.0% (0.0-1.5%)		
gtm127	17.3%	x 0.06	x 11.1	2.6	XX	H1a3a	-	>25.3k	0.0% (0.0-22.1%)		
kal006	56.0%	x 1.2	x 87	1.0	XX	V7a	-	>278.6k	0.4% (0.0-1.27%)		
kal009	1.6%	x 0.19	x 124.4	17.6	XX	T2f1	-	>71k	0.32% (0.0-0.67%)		
kls001	18.1%	x 0.13	x 11.8	4.4	XY	H1b1	R1*	>53.3k	0.0% (0.0-22.09%)	0.00372 (0.001858)	0.00204 (0.001491)
nuf002	52.7%	x 0.16	x 44.1	2.4	XY	T1a1j	Nd	>66.4k	0.5% (0.0-1.3%)	0.00179 (0.001393)	0.00013 (0.000217)
stg020	4.5%	x 0.18	x 59.4	66.9	XX	T2	-	>73.1k	0.23% (0.0-0.69%)		
stg021	46.4%	x 3.4	x 136	28.0	XX	J1d1b1	-	>366.8k	0.57% (0.07-1.07%)		
stg026	6.4%	x 0.61	x 367.2	16.3	XX	J1c2k	-	>189.1k	0.18% (0.04-0.33%)		
urm035	3.1%	x 0.26	x 240.3	18.1	XY	H2a1c	BCDEF	>95.2k	0.35% (0.0-0.69%)	0.00229 (0.001346)	0.00104 (0.001095)
urm045	1.7%	x 0.09	x 74.7	47.1	XY	H1a8	Nd	>38.3k	0.0% (0.0-1.55%)	6.61E-05 (0)	6.61E-05 (0)
urm160	17.8%	x 1.3	x 299	16.3	XY	H1q	R1b1a1a2a1	>295.3k	0.13% (0.0-0.39%)	0.00757 (0.000817)	0.00548 (0.000860)
urm161	1.1%	x 0.08	x 19.6	30.6	XY	T1 (40%)	A2'3'4	>34.6k	0.0% (0.0-1.67%)	0.00463 (0.002544)	0.00188 (0.001586)

Table S3. Summary statistics of genomic analyses for sampled individuals. Related to Figure 2 and Table 1.

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